



## Blast 2 Sequences results

PubMed

Entrez

**BLAST**

OMIM

## Taxonomy

## Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]**

Match: 1      Mismatch: -2      gap open: 5      gap extension: 2

x dropoff: 0 expect: 10.000 wordsize: 11 Filter ☐ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

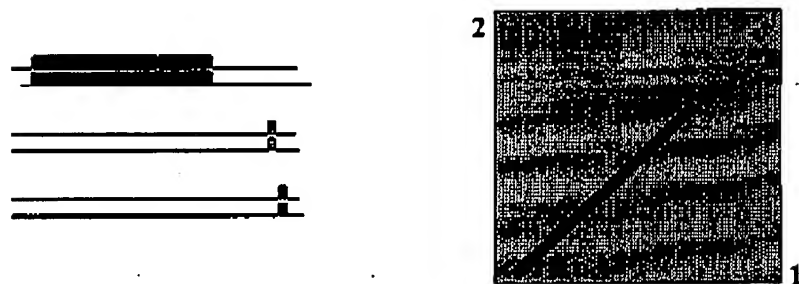
 Show CDS translation

**Sequence 1: lcl|seq 1**

Length = 4867 (1 .. 4867)

**Sequence 2: lcl|seq 2**

Length = 4936 (1 .. 4936)



**NOTE:**Bitscore and expect value are calculated based on the size of the nr database.

**NOTE:**If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

**EXHIBIT**

4

Score = 3012 bits (1566), Expect = 0.0  
Identities = 2570/3067 (83%), Gaps = 6/3067 (0%)  
Strand=Plus/Plus

[illegible]

## Blast Result

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Query	537	AAGCTCGAGTGCCTGGTGTATTCTCTGTAAATACAGTTTATTATGAGAACACAGGGGCGC	596
Sbjct	369	AAATCCAAGGGTCCGATGTTATTCTTACAAATACAATTTATAACCAGAGCACTGTGGTGT	428
Query	597	CCTCTCTGCCCCCAGCCAGTCCACTCCAGCCTGGACACCGAGAGCTCCTTCTCCAGAGG	656
Sbjct	429	CTACTGCACATCCCGACCAACACGTTCCAGCCTGGACTACGGATGCTTCTCTCCCAGGGG	488
Query	657	ACCAGAGTCACAGGAACACAAGCACCTGCATGAACATCACTCACAGCCAGTGTCAAATTC	716
Sbjct	489	ACCAAAGTCACAGGAATACAAGTGCTGTATGAACATCACCCACAGCCAGTGTGAGATGC	548
Query	717	TGCCCTACCACAGCACGTTGGCACCTCTCTTGCCAATTGTCAAAAACATGGACATGGAGA	776
Sbjct	549	TGCCCTACCAGCCACGCTGACACCTCTCCTCTCAGTTGTGAGAAACATGGAAATGGAAA	608
Query	777	AGTTCTCTCAAGTTCTTCACGTACCTCCATCGCCTCAGTTGCTATCAACATATCCTGCTCT	836
Sbjct	609	AGTTCTCTCAAGTTTTCACATATCTCCATCGCCTCAGTTGCTATCAACATATCATGCTGT	668
Query	837	TCGGCTGTAGCCTCGCCTTCCCTGAGTGCCTTGTGATGGCGATGACAGGCATGGTCTTC	896
Sbjct	669	TTGGCTGTACCCTCGCCTTCCCTGAGTGCATCATTGATGGCGATGACAGTCATGGACTCC	728
Query	897	TACCCTGTAGATCTTTCTGTGAGGCTGCAAAAGAAGGATGCGAATCTGTCTCTGGGAATGG	956
Sbjct	729	TGCCCTGTAGGTCCTTCTGTGAGGCTGCAAAAGAAGGCTGTGAATCAGTCCTGGGGATGG	788
Query	957	TGAACTCCTCCTGGCCGGATTCCCTCAGATGCTCTCAGTTTAGGGACCACACTGAGACTA	1016
Sbjct	789	TGAATTACTCCTGGCCGGATTTCCTCAGATGCTCCCAGTTTAGAAACCAAATGAAAG---	846
Query	1017	ACAGCAGTGTGAGAAAGAGCTGCTTCTCACTGCAGCAGGAACATGGAAAGCAATCACTCT	1076
Sbjct	847	-CAGCAATGTGAGCAGAAATTTGCTTCTCACCTCAGCAGGAAAACGAAAGCAATTGCTCT	905
Query	1077	GTGGAGGGGGGCGAGAGCTTCTGTGTACAGCGGGCTCTGCGTCCCCAAGAAGCTGCAGT	1136
Sbjct	906	GTGGAAGGGGTGAGAACTTTCTGTGTGCCAGTGAATCTGCATCCCCGGGAAACTGCAAT	965
Query	1137	GTAACGGCTATAATGACTGTGATGACTGGAGCGACGAGGCGCATTGCAACTGCAGCAAGG	1196
Sbjct	966	GTAATGGCTACAACGACTGTGACGACTGGAGTGACGAGGCTCATTGCAACTGCAGCGAGA	1025
Query	1197	ATCTGTTTCACTGTGGCACAGGCAAGTGCCCTCACTACAGCCTCTGTGTGATGGGTACG	1256
Sbjct	1026	ATCTGTTTCACTGTGACACAGGCAAGTGCCCTTAATTACAGCCTTGTGTGATGGATATG	1085
Query	1257	ATGACTGTGGGGACCCGAGTGACGAGCAAACTGTGATTGTAATCTCACAAAAGAGCATC	1316
Sbjct	1086	ATGACTGTGGGGATTTGACTGATGAGCAAACTGTGATTGCAATCCCACAACAGAGCATC	1145
Query	1317	GCTGTGGAGATGGGCGCTGCATTGCGGCTGAGTGGGTGTGCGATGGGGACCATGACTGTG	1376
Sbjct	1146	GCTGCGGGGACGGGCGCTGCATCGCCATGGAGTGGGTGTGTGATGGTGACCACGACTGTG	1205
Query	1377	TGGACAAGTCTGATGAGGTCAACTGCTCTTGTACAGCCAGGGCCTGGTGGAATGCACAA	1436
Sbjct	1206	TGGATAAGTCCGACGAGGTCAACTGCTCCTGTACAGCCAGGGTCTGGTGGAATGCAGAA	1265

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PAGE 8/13 \* RCVD AT 4/24/2007 4:47:37 PM [Eastern Daylight Time] \* SVR:USPTO-EFXRF-1/15 \* DNIS:2738300 \* CSID:415 576 0300 \* DURATION (mm:ss):04:46/18/2007

## Blast Result

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Query	2337	GTGTGACCCCTCTCTAAAAATGGGAACCTCCTCCTCATTGCTGACTGTTTACAAAATCTGCAA	2396
Sbjct	2166	GTGTGACCCCTCTCTATAAATGTGAACTCCTCTTCTTCTGATGGTTTACAGAGCTGCCA	2225
Query	2397	AGGAACACCACGTTGTGTGCTGACGGCTGGCGGGAGACGTTGAGTCAGCTGGCCTGCAAGC	2456
Sbjct	2226	CAGAACACCATGTGTGTGTCAGATGGCTGGCAGGAGATATTGAGTCAGCTGGCCTGCAAGC	2285
Query	2457	AGATGGGTTTtaggagaaccgtctgtgaccaagctgatcccaggacagg---aaggccagc	2513
Sbjct	2286	AGATGGGTTTtaggagaaccatctgtgaccAAATTGATACAGGAACAGGAGAAAGAGCCGC	2345
Query	2514	AGTGGCTGAGGTTGTACCCCAACTGGGAGAATCTCAATGGGAGCACCTTGCAAGGAGCTGC	2573
Sbjct	2346	GGTGGCTGACATTACACTCCAAGTGGGAGAGCCTCAATGGGACCACCTTACATGAACCTTC	2405
Query	2574	TGGTATACAGGCACCTCTGCCCCAAGCAGAAGTGAGATTTCCCTTCTGTGCTCCAAGCAAG	2633
Sbjct	2406	TAGTAAATGGGCAGTCTTGTGAGAGCAGAAGTAAATTTCTCTTCTGTGTACTAAACAAG	2465
Query	2634	ACTGTGGCCGCCGCCCTGCTGCCCCGAATGAACAAGAGGATCCTTGGGGGTCCGACTAGTC	2693
Sbjct	2466	ACTGTGGCCGCCGCCCTGCTGCCCCGAATGAACAAAAGGATCCTTGGAGGTCCGACGAGTC	2525
Query	2694	GTCTTGGGAGGTGGCCGTGGCAGTGCTCTCTGCAGAGTGAACCCAGTGGACATATCTGTG	2753
Sbjct	2526	CCCCTGGAAGGTGGCCATGGCAGTGTTCTCTGCAGAGTGAACCCAGTGGACATATCTGTG	2585
Query	2754	GCTGTGTCCTCATTGCCAAGAAGTGGGTCTCTGACAGTTGCCCATTTGCTTTGAAGGGAGAG	2813
Sbjct	2586	GCTGTGTCCTCATTGCCAAGAAGTGGGTCTCTGACAGTTGCCCATTTGCTTTGAGGGGAGAG	2645
Query	2814	AAGACGCTGATGTTTGGAAAGTGGTATTTGGCATAAACAACCTGGACCATCCATCAGGCT	2873
Sbjct	2646	AGAATGCTGCAGTTTGGAAAGTGGTGCTTGGCATCAACAATCTAGACCATCCATCAGTGT	2705
Query	2874	TCATGCAGACCCGCTTTGTGAAGACCATCCTGCTACATCCCCGTTACAGTCGAGCAGTGG	2933
Sbjct	2706	TCATGCAGACACGCTTTGTGAAGACCATCATCCTGCATCCCCGCTACAGTCGAGCAGTGG	2765
Query	2934	TAGACTATGATATCAGCGTGGTGGAGCTGAGCGATGATATCAATGAGACAAGCTACGTCA	2993
Sbjct	2766	TGGACTATGACATCAGCATCGTTGAGCTGAGTGAAGACATCAGTGAGACTGGCTACGTCC	2825
Query	2994	GACCTGTCTGCCTACCCAGTCCGGAGGAGTATCTAGAACCAGATACGTACTGCTACATCA	3053
Sbjct	2826	GGCCTGTCTGCTTGCCCCAACCCGAGCAGTGGCTAGAGCCTGACACGTACTGCTATATCA	2885
Query	3054	CAGGCTGGGGCCACATGGGCAATAAAATGCCCTTTAAGCTGCAGGAGGGAGAGGTCCGCA	3113
Sbjct	2886	CAGGCTGGGGCCACATGGGCAATAAAATGCCATTTAAGCTGCAAGAGGGAGAGGTCCGCA	2945
Query	3114	TTATCCCTCTGGAGCAGTGCCAGTCTTATTTTGACATGAAGACCATCACCAATCGGATGA	3173
Sbjct	2946	TTATTTCTCTGGAACATTGTCACTCTTACTTTGACATGAAGACCATCACCACTCGGATGA	3005
Query	3174	TCTGTGCTGGCTATGAGTCTGGCACCGTGGACTCCTGCATGGGAGACAGCGGTGGGCCTC	3233
Sbjct	3006	TATGTGCTGGCTATGAGTCTGGCACAGTTGATTTCATGCATGGGTGACAGCGGTGGGCCTC	3065

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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 0 expect: 10.000 wordsize: 3 Filter: View option: Standard  
 Masking character option: X for protein, n for nucleotide Masking color option: Black  
☐ Show CDS translation

Sequence 1: lcl|seq\_1  
 Length = 1113 (1 .. 1113)

Sequence 2: lcl|seq\_2  
 Length = 1042 (1 .. 1042)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

EXHIBIT

B

Score = 1658 bits (4293), Expect = 0.0, Method: Composition-based stats.  
 Identities = 849/1023 (82%), Positives = 921/1023 (90%), Gaps = 2/1023 (0%)

Query	86	PAPDVLRADRSVGEGCPQKLVTANLLRFLLLVLIPICICALIVLLAILLSFVGTALKRVYFK	145
		P P + D ++G GC QKL TANLLRFLLLVLIPICICAL++LL ILLS+VGTL++VYFK	
Sbjct	19	PKPVLRADDDNMMGNGCSQKLATANLLRFLLLVLIPICICALVLLLVILLSYVGTALQKVYFK	78
Query	146	SNDSEPLVTDGEARVPGVIPVNTVYYENTGAPSLPPSQSTPAWTFRAPSPEDQSHRNTST	205
		SN SEPLVTDGE + VI NT+Y ++T + P Q PAWT A P DQSHRNTS	
Sbjct	79	SNGSEPLVTDGEIQSDVILTNTIYNQSTTVVSTAHPDQHPAWTTDASLPGDQSHRNTSA	138
Query	206	CMNITHSQCQILPYHSTLAPLLPIVKNMDMEKFLKFFTYLHRLSCYQHILLFGCSLAFPE	265
		CMNITHSQCQ+LPYH+TL PLL +V+NM+MEKFLKFFTYLHRLSCYQHI+LFGC+LAFPE	
Sbjct	139	CMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHRLSCYQHIMLFGCTLAFPE	198
Query	266	CVVDGDDRHGLLPCRFSFCEAAKEGCESVLGMVNSSWPD SLRCSQPRDHTETNSSVRKSCF	325
		C++DGDD HGLLPCRFSFCEAAKEGCESVLGMVN SWPD LRCSQPR+ TE+ S+V + CF	
Sbjct	199	CIIDGDDSHGLLPCRFSFCEAAKEGCESVLGMVNSWPD FLRCSQPRNOTES-SNVSRI CF	257

## Blast Result

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Query	326	SLQQEHGKQSLCGGGESFLCTSGLCVPKKLQCNGYNDCCDDWSDEAHCNCSKDLFHC GTGK	385
		S QQE+GKQ LCG GE+FLC SG+C+P KLQCNGYNDCCDDWSDEAHCNCS++LFHC TGK	
Sbjct	258	SPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCCDDWSDEAHCNCS ENLFHC HTGK	317
Query	386	CLHYSLLCDGYDDCGDPSDEQNCDCNLTKEHRCGDGRCIAAEWVCDGDHDCVDKSDDEVNC	445
		CL+YSL+CDGYDDCGD SDEQNCDCN T EHRCGDGRCLAEWVCDGDHDCVDKSDDEVNC	
Sbjct	318	CLNYSLVCDGYDDCGDLSDQNCDCNPTTEHRCGDGRCIAEWEVCDGDHDCVDKSDDEVNC	377
Query	446	SCHSQGLVECTSGQCIPSTFQCDGDEDCKDGSDEENCSDSQTPCPEGEQGC FGSSCVESC	505
		SCHSQGLVEC +GQCIPSTFQCDGDEDCKDGSDEENC S QT C EG+Q C + C++SC	
Sbjct	378	SCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENC SVIQTSCQEGDQRCLYNPCLDSC	437
Query	506	AGSSLCDSDSSLSNCSQCEPITL ELCMNLLYNH THYPNYLGHRTQKEASISWESSLPAL	565
		GSSLCD++SL+NCSQCEPITL ELCMN L YN T YPNY GHRTQKEASISWESSLPAL	
Sbjct	438	GGSSLCDPNNLSNCSQCEPITL ELCMNLPYNSTSYPNYFGHRTQKEASISWESSLPAL	497
Query	566	VQTNCYKYLMMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCESVLGIVGLQWPEDTDC	625
		VQTNCYKYLMMFF+CTILVPKCDVNTG+RIPPCR LCEHSKERCESVLGIVGLQWPEDTDC	
Sbjct	498	VQTNCYKYLMMFFSCTILVPKCDVNTGERIPPCRALCEHSKERCESVLGIVGLQWPEDTDC	557
Query	626	NQFPPESSDNQTCLLPNEDVEECSPSHFKCRSGRCVLSRRCDGQADCCDDSD EENC CGCK	685
		+QFPPE+SDNQTCL+P+E VEECSPSHFKCRSG+CVL SRRCDGQADCCDDSD EENC CGCK	
Sbjct	558	SQFPPESSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCDGQADCCDDSD EENC CGCK	617
Query	686	ERALWECFPFNKQCLKHTLICDGFDPDCPD SMDEKNCSFCQDNELECANHECVPRDLWCDGW	745
		ER LWECF NKQCLKHT+ICDGFDPDCPD MDEKNCSFCQD+ELECANH CV RDLWCDG	
Sbjct	618	ERDLWECFSPNKQCLKHTVICDGFDPDCPDYMD EKNCSFCQDDELECANHACVSRDLWCDGE	677
Query	746	VDCSDSSDEWGCVTLSKNGNSSLLTVHKSABEHVHCADGWRETLSQLACKQMGLGEP SV	805
		DCSDSSDEW CVTLS N NSSS L VH++A EHVHCADGW+E LSQLACKQMGLGEP SV	
Sbjct	678	ADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHVHCADGWQEILSQLACKQMGLGEP SV	737
Query	806	TKLIPQGEQ-QWLRLYPNWNENLNGSTLQELLVYRHSCPSRSEISLLCSKQDCGRRPAAR	864
		TKLI QE + +WL L+ NWE+LNG+TL ELLV SC SRS+ISLLC+KQDCGRRPAAR	
Sbjct	738	TKLIQEKEKEPRWLTLSHNSWESLNGTTLHELLVNGQSCESRSKISLLCTKQDCGRRPAAR	797
Query	865	MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGREDADVWKVV	924
		MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRE+A VWKVV	
Sbjct	798	MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRENAAVWKVV	857
Query	925	FGINNLDHPSGFMQTRFVKTIILHPRYSRAVDYDISVVELSDDINETS YVRPVCLPSP E	984
		GINNLDHPS FMQTRFVKTI+LHPRYSRAVDYDIS+VELS+DI+ET YVRPVCLP+PE	
Sbjct	858	LGINNLDHPSVFMQTRFVKTIILHPRYSRAVDYDISIVELSEDISETG YVRPVCLPNPE	917
Query	985	EYLEPDTYCYITGWGHMGNMKMPFKLQEGEVRIIPLQCQSYFDMKTIITNRMICAGYESGT	1044
		++LEPDTYCYITGWGHMGNMKMPFKLQEGEVRII LE CQSYFDMKTIIT RMICAGYESGT	
Sbjct	918	QWLEPDTYCYITGWGHMGNMKMPFKLQEGEVRIISLEHCQSYFDMKTIITRMICAGYESGT	977
Query	1045	VDSCMGDSGGPLVCERP GGQWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVGWIERQIYIQ	1104
		VDSCMGDSGGPLVCE+PGG+WTLFGLTSWGSVCFSKVLGPGVYSNVSYFV WI+RQIYIQ	
Sbjct	978	VDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVEWIKRQIYIQ	1037
Query	1105	TFL 1107	
		TFL	
Sbjct	1038	TFL 1040	

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.